SFQ ID NO.1 FIG.1 a

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59(U.PER:SER I) NO 19(LOWER:SER ID NO4
TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA	239 79
	299
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	99
MDYQVSSPIYDINYYTSEPC	99
	359
CALLAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	
G K I N V K Q I A A R L L P P L Y S L V	119
TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	419
F I F G F V G N M L V I L I N C K R	139
The same and the same action of the same actions of the same actio	479
CTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	159
H K S M T D I Y L L N L A I S D L F F L	
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG	539
HTVPFWAHYAAAQWDFGNTM	179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
	199
CFCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG	659
LLTIDRYLAVVHAVFALKAR	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGTGTGTTTGCGTCT	719
- 	239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259

CATTITCCATACA H F P Y

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59 (UPPERISER I) NO Z 19 (ISWER SEA I) NO S
TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGCCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA	239 79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC M D Y Q V S S P I Y D I N Y Y T S E P C	299 99
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG O K I N V K Q I A A R L L P P L Y S L V	359 119
TCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG F I F G F V G N M L V I L I L I N C K R	419 139
GTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT L K S M T D I Y L L N L A I S D L F F L	479 159
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG CL T V P F W A H Y A A A Q W D F G N T M U	539 179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC CC Q L L T G L Y F I G F F S G I F F I I	599 199
CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTTTTGCTTTAAAAGCCAGG L L T I D R Y L A V V H A V F A L K A R	659 219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTTTTGCGTCT T V T F G V V T S V I T W V V A V F A S	719 239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT L P G I I F T R S Q K E G L H Y T C S S	779 259
CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC H F P Y S Q Y Q F W K N F Q T L K I V I	839 279

SEQ ID NO.2 FIG.1b

TTG	GGG	CTG	GTC	CTC	CCG	CTG	CTI	GTC	'ATC	GTC	ATC	TGC	TAC	TCG	GGA	ATC	CTA	AAA	ACT	899
$\mathbf{L}_{_{q}}$	G	L	Λ	L	P	L	L	V	M	Λ	I	С	Y	S	G	I	Ŀ	K	T	299
CTG	CTI	'CGG	TGT	'CGA	AAT	'GAG	AAC	AAG	AGG	CAC	AGG	GCI	GTG	AGG	CTI	'ATC	TIC	ACC	ATC	959
L	L	R	С	R	N	Ε	K	K	R	H	R	A	V	R	L	I	F	Т	I	319
ATG	ATT	GTI	TAT	TTI	CTC	TTC	TGG	GCT	CCC	TAC	AAC	ATT	GTC	CTI	'CTC	CTG	AAC	ACC	TTC	1019
М	I	V	Y	F	L	F	M	A	P	Y	N	I	V	L	L	L	N	T	F	339
CAG	GAA	TTC	TIT	GGC		AAT	AAT	TGC	AGI				AGG	TTG	GAC	CAA	GCT	ATG	CAG	1079
Q	E	F	F	G	L	N	N	С	S	S	S	N	R	L	D	Q	A	M	Q	359
GTG	ACA	GAG	ACT	CIT	GGG	ATG	ACG			TGC	ATC	AAC	CCC	ATC	ATC	TAT	GCC	TIT	GTC	1139
V	T	E	T	L	G	M	T	H	С	С	I	N	P	I	Ι	Y	A	F	V	379
GGG	GAG	AAG	TTC	AGA	AAC	TAC	CTC	TTA	GTC	TTC	TTC	CAA	AAG	CAC	ATT	GCC	AAA	CGC	TTC	1199
G	E	K	F	R	N	Y	L	L	V	F	F	Q	K	H	I	A	K	R	F	399
TGC	AAA	TGC	TGT	TCT	ATT	TTC	CAG	CAA	GAG	GCT	CCC	GAG	CGA	GCA	AGC	TCA	GTT	TAC	ACC	1259
C	K	C	С	S	I	F	Q	Q	E	A	P	E	R	A	S	S	V	Y	T	419
CGA'	TCC	ACT	GGG	GAG	CAG	GAA	ATA	TCT	GTG	GGC	TTG	TGA	CAC	GGA	CTC	AAG	TGG	GCT	GGT	1319
R	S	T	G	E	Q	E	I	S	Λ	G	L	*								439
GAC 10	CCA	GTC	AGA	GTT	GTG	CAC	ATG	GCT	TAG	TTT	TCA	TAC	ACA	GCC	TGG	GCT	GGG	GGT	NGG	1379 459
TIG	GNN	GAG	GTC'	TTT	TTT.	AAA	AGG.	AAG	TTA	CTG'	TTA	TAG.	AGG	GTC	TAA	GAT	TCA'	TCC	ATT	1439 479
8																				
TAT	FTG	GCA'	TCT	GTT	TAA	AGT.	AGA'	TTA	GAT	CCG.	AAT	TC								
that there is find																				
That with																				
S. Calle																				

SEQ ID NO.2 (SUITE)

FIG.1c

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	5 KUPPER: SER II) ND 3 19 (LOWER: SER II) ND 6
TTCCCTTCACTACAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA	239 79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359
Q K I N V K Q I A A R L L P P L Y S L V	119
	223
TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	419
FIFGFVGNMLVILILINCKR	139
@TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
	159
L K S M T D I Y L L N L A I S D L F F L	
ETTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG	539
L T V P F W A H Y A A A Q W D F G N T M	179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
COLLTGLY FIGFFS G. I FFI I	199
CQLLTGLYFIGFFSG·IFFII	
TTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG	659
LLTIDRYLAVVHAVFALKAR	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTTTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
TATEGAATOATINAAVE	
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259
CATTTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGT	839
H F P Y I K D S H L G A G P A A A C H G	279

SEQ ID NO.3

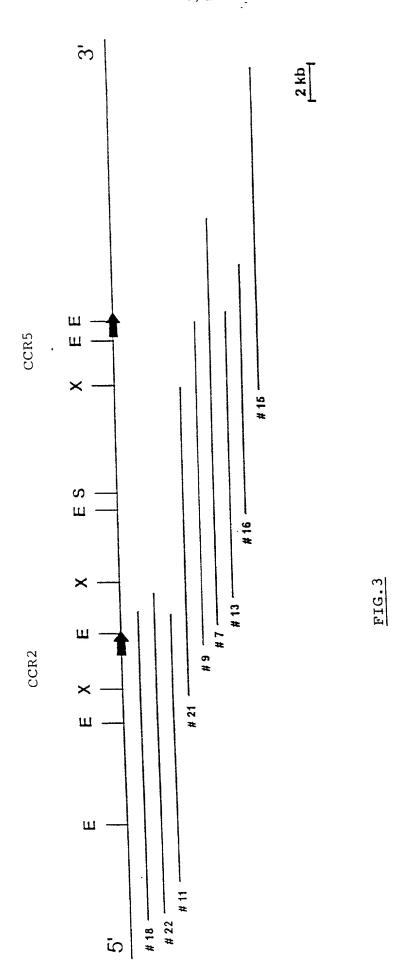
FIG.1d

CATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCA H L L L G N P K N S A S V S K *	899 299
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTA	959 319
CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG	1019 339
CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG	1079 359
CATCAACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTT	1139 379
CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC	1199 399
TCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG	1259 419
COTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT	1319 439
TCATACACAGCCTGGGCTGGGGTNGGTTGGNNGAGGTCTTTTTTAAAAGGAAGTTACT	1379 459
GTTATAGAGGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC	1439 479
ून ब्याह्म अ. इ. <u>क</u>	

SEQ ID NO.3 (SUITE)
 FIG.1e

FIG. 2

		. " ~	
1 METQUSSPIPPINYTSEPCORINVKOINARLIPPLYSIVETEGEVGNMINTITINCKRIKSMTDIYLINIATSDIRFINT 83 nettsichtertrydygapenkethethelysinetegevgnmintikynnirikynlitiniatsdirfint 95 metpattedydttefengenkethethelysinentysinentysinentynnirikynnirikynlitiniatsdirfielti 87 metpattedydttefengentegenkegikagikagikagilagentysinentys	VEFWAIIYA BAQWOEGNIMOOLLTGI.YEIGEESGIFETIILTIDRYLANVIIAVEALKARTVTEGVVTSVITWIVAVEASLEGIIETIRGKEGI[] 177 LELWAIISA BAEWVEGNAMOKI ETGI.YIIIGYETSIFETIILTIDRYLANVIIAVEALKARTVTEGVVTSVITWIVAVEASIPEGIIETIETIETIETIETIETIETIETIETIETIETIETIET	YTCHERESOVOEWKNEOTLKIJVITGLVI.PI.I.VMVICYSGII.KTI.I.RCRNEKKRHRAVRI.I ETIMIVYEI YTCHEREN SQYQEWKNEOTLKIJVITGLVI.PI.I.VMVICYSGII.KTI.I.RCRNEKKRHRAVRI.I ETIMIVYEI YTCHEREN SQYQEWKNEOTLKIJVITGLVI.PI.I.VMVICYSGII.KTI.I.RCRNEKKRHRAVRVI.EVIMAVEPT YTCHEREN SQYQEWKLEOTLKINI.EGLVI.PI.I.VMIICYNGII.KTII.LRRENEKK. SKAVRI.I.EVIMII.EEI TYCKTKYSI.NST.TWKVI.SSI.EIINII.GI.VITEIGIIMI.ECYSMIIRRII.ZHCKNEKK. NKAVKMI.EAVVVI.EI.G	SSSHIR DOAROVTETLGE ERFRU DOAROVTETLGE ECERTION ANOVTEVIA TFERYLDYANDARETIA
CCR5 hcc-R2b hcc-R3 hcc-R1	ccR5 hcc-R2b hcc-<3 hccP1 hccR4	ccR5 ncc-R2b ncc-R3 ncc-R1	ccrs hcc-r2b hcc-r3 hcc- R1 hcc- R4



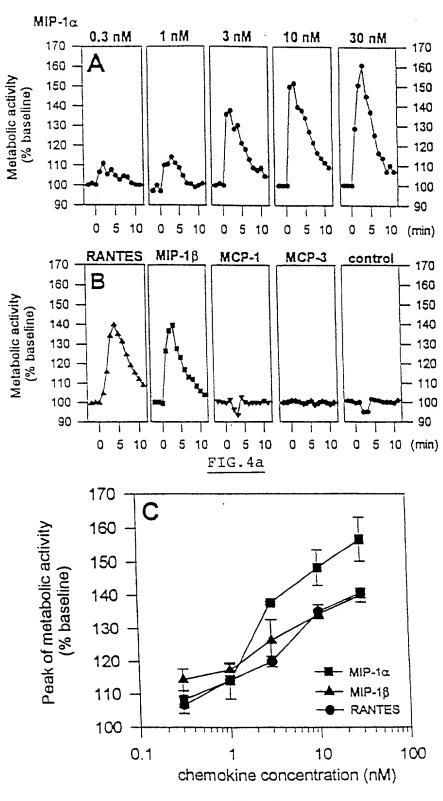


FIG.4b

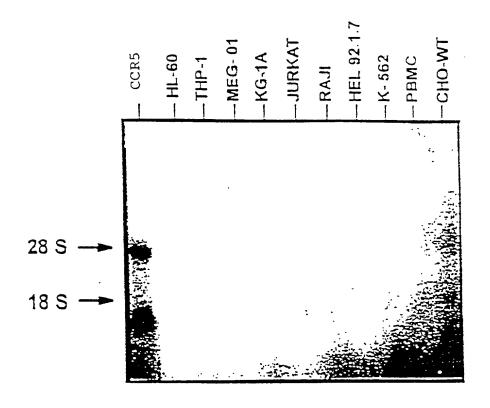
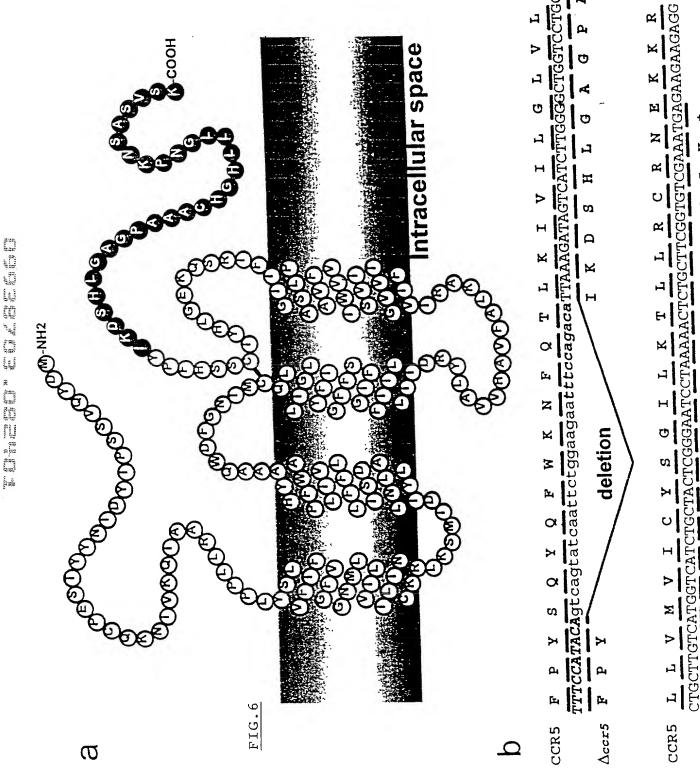
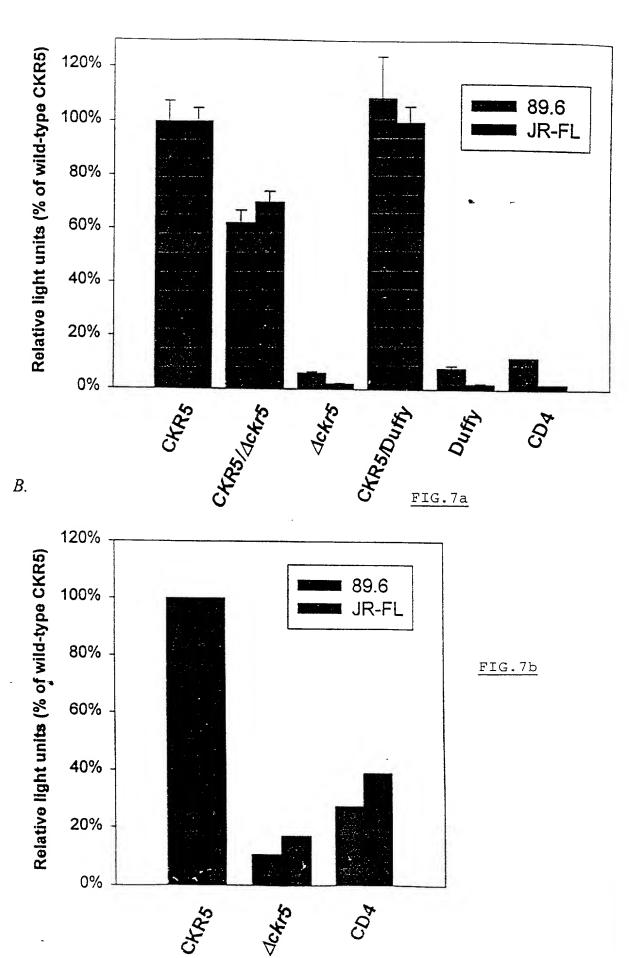


FIG.5







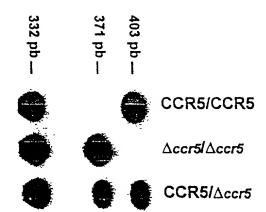
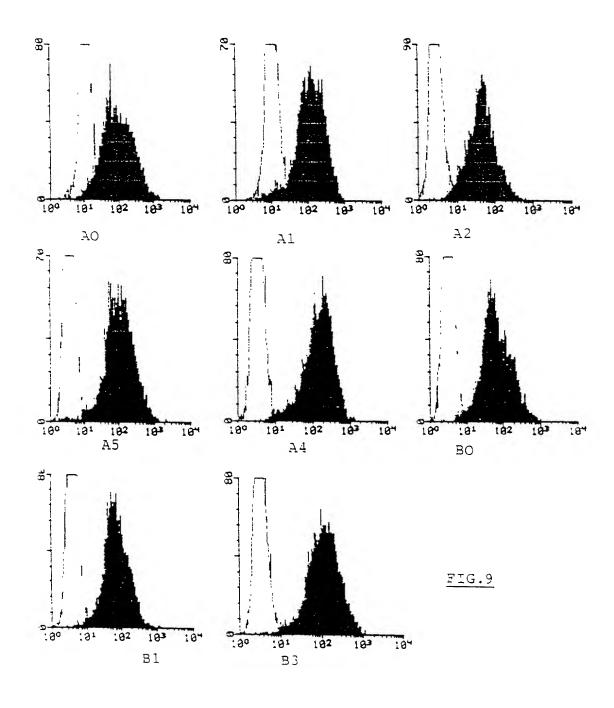


FIG.8



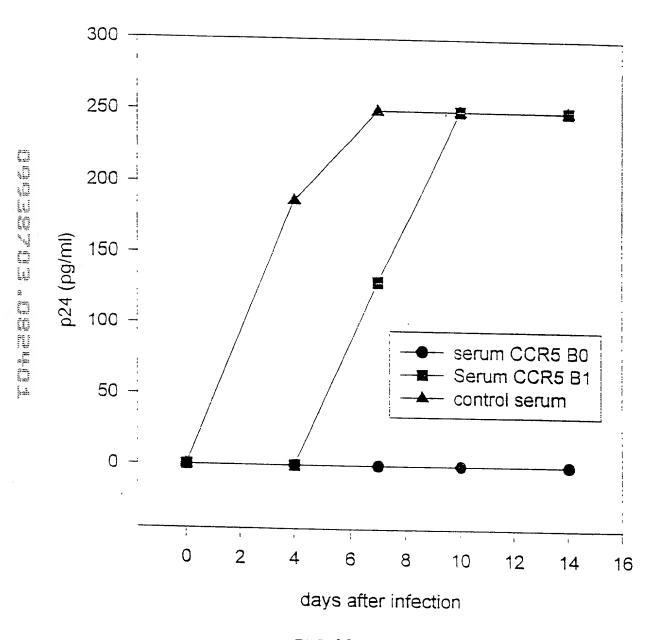


FIG.10